RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/808,121A**

DATE: 08/06/2004
TIME: 14:27:47

Input Set : **D:\V9661069.app**
Output Set: **N:\CRF4\08062004\J808121A.raw**

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 3 <110> APPLICANT: PEIRIS, JOSEPH S. M.
 4        YUEN, KWOK YUNG
 5.       POON, LIT MAN
 6        GUAN, YI
 7        CHAN, KWOK HUNG
 8        NICHOLLS, JOHN
10 <120> TITLE OF INVENTION: NOVEL HUMAN VIRUS CAUSING SEVERE ACUTE RESPIRATORY SYNDROME
11        (SARS) AND USES THEREOF
13 <130> FILE REFERENCE: V9661.0069
15 <140> CURRENT APPLICATION NUMBER: 10/808,121A
16 <141> CURRENT FILING DATE: 2004-03-24
18 <150> PRIOR APPLICATION NUMBER: 60/457,031
19 <151> PRIOR FILING DATE: 2003-03-24
21 <150> PRIOR APPLICATION NUMBER: 60/457,730
22 <151> PRIOR FILING DATE: 2003-03-26
24 <150> PRIOR APPLICATION NUMBER: 60/459,931
25 <151> PRIOR FILING DATE: 2003-04-02
27 <150> PRIOR APPLICATION NUMBER: 60/460,357
28 <151> PRIOR FILING DATE: 2003-04-03
30 <150> PRIOR APPLICATION NUMBER: 60/461,265
31 <151> PRIOR FILING DATE: 2003-04-08
33 <150> PRIOR APPLICATION NUMBER: 60/464,886
34 <151> PRIOR FILING DATE: 2003-04-23
36 <160> NUMBER OF SEQ ID NOS: 2470
38 <170> SOFTWARE: PatentIn ver. 3.2
40 <210> SEQ ID NO: 1
41 <211> LENGTH: 646
42 <212> TYPE: DNA
43 <213> ORGANISM: Human severe acute respiratory syndrome virus
45 <220> FEATURE:
46 <221> NAME/KEY: CDS
47 <222> LOCATION: (2)...(646)
49 <400> SEQUENCE: 1
50 a cag gac gct gta gct tca aaa atc tta gga ttg cct acg cag act gtt  49
51   Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
52    1               5                   10                  15
54 gat tca tca cag ggt tct gaa tat gac tat gtc ata ttc aca caa act      97
55 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr
56               20                  25                  30
58 act gaa aca gca cac tct tgt aat gtc aac cgc ttc aat gtg gct atc     145
59 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile
60           35                  40                  45
62 aca agg gca aaa att ggc att ttg tgc ata atg tct gat aga gat ctt     193
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63 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu
64      50                  55                  60
66 tat gac aaa ctg caa ttt aca agt cta gaa ata cca cgt cgc aat gtg    241
67 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val
68  65                  70                  75                  80
70 gct aca tta caa gca gaa aat gta act gga ctt ttt aag gac tgt agt    289
71 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser
72                  85                  90                  95
74 aag atc att act ggt ctt cat cct aca cag gca cct aca cac ctc agc    337
75 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser
76                  100                 105                 110
78 gtt gat ata aaa ttc aag act gaa gga tta tgt gtt gac ata cca ggc    385
79 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly
80          115                 120                 125
82 ata cca aag gac atg acc tac cgt aga ctc atc tct atg atg ggt ttc    433
83 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe
84      130                 135                 140
86 aaa atg aat tac caa gtc aat ggt tac cct aat atg ttt atc acc cgc    481
87 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg
88 145                 150                 155                 160
90 gaa gaa gct att cgt cac gtt cgt gcg tgg att ggc ttt gat gta gag    529
91 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu
92                  165                 170                 175
94 ggc tgt cat gca act aga gat gct gtg ggt act aac cta cct ctc cag    577
95 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln
96                  180                 185                 190
98 cta gga ttt tct aca ggt gtt aac tta gta gct gta ccg act ggt tat    625
99 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr
100         195                 200                 205
102 gtt gac act gaa aat aac cta                                        646
103 Val Asp Thr Glu Asn Asn Leu
104     210                 215
107 <210> SEQ ID NO: 2
108 <211> LENGTH: 215
109 <212> TYPE: PRT
110 <213> ORGANISM: Human severe acute respiratory syndrome virus
112 <400> SEQUENCE: 2
113 Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
114 1               5                   10                  15
116 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr
117             20                  25                  30
119 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile
120         35                  40                  45
122 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu
123     50                  55                  60
125 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val
126 65                  70                  75                  80
128 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser
129                 85                  90                  95
```

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Input Set : **D:\V9661069.app**
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```
131 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser
132             100                 105                 110
134 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly
135         115                 120                 125
137 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe
138     130                 135                 140
140 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg
141 145                 150                 155                 160
143 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu
144                 165                 170                 175
146 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln
147             180                 185                 190
149 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr
150             195                 200                 205
152 Val Asp Thr Glu Asn Asn Leu
153     210                 215
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 17
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial
163       nucleotide sequence of the gemome of hSARS
165 <400> SEQUENCE: 3
166 tacacacctc agcgttg                                              17
168 <210> SEQ ID NO: 4
169 <211> LENGTH: 16
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial
175       nucleotide sequence of the gemome of hSARS
177 <400> SEQUENCE: 4
178 cacgaacgtg acgaat                                               16
180 <210> SEQ ID NO: 5
181 <211> LENGTH: 27
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: degenerated primer in Superscript II Kit by
187       Invitrogen
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: (21)..(27)
192 <223> OTHER INFORMATION: a, t, c or g
194 <400> SEQUENCE: 5
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W--> 195 gccggagctc tgcagaattc nnnnnnn   27
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197 <210> SEQ ID NO: 6
198 <211> LENGTH: 20
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RAW SEQUENCE LISTING   DATE: 08/06/2004
PATENT APPLICATION: **US/10/808,121A**   TIME: 14:27:47

Input Set : **D:\V9661069.app**
Output Set: **N:\CRF4\08062004\J808121A.raw**

```
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: primer provided in AmpliTaq Gold Kit by Applied
204        Biosyndromes
206 <400> SEQUENCE: 6
207 gccggagctc tgcagaattc                                    20
209 <210> SEQ ID NO: 7
210 <211> LENGTH: 17
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: First round of primer for amplifying human
216        metapneumovirus (HMPV)
218 <400> SEQUENCE: 7
219 aargtsaatg catcagc                                       17
221 <210> SEQ ID NO: 8
222 <211> LENGTH: 20
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: first round primer for amplifying human
228        metapneumovirus (HMPV)
230 <400> SEQUENCE: 8
231 cakattytgc ttatgctttc                                    20
233 <210> SEQ ID NO: 9
234 <211> LENGTH: 20
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus
240        (HMPV)
242 <400> SEQUENCE: 9
243 acacctgtta caataccagc                                    20
245 <210> SEQ ID NO: 10
246 <211> LENGTH: 19
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus
252        (HMPV)
254 <400> SEQUENCE: 10
255 gacttgagtc ccagctcca                                     19
257 <210> SEQ ID NO: 11
258 <211> LENGTH: 1213
259 <212> TYPE: DNA
260 <213> ORGANISM: Human severe acute respiratory syndrome virus
262 <220> FEATURE:
263 <221> NAME/KEY: CDS
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RAW SEQUENCE LISTING   DATE: 08/06/2004
PATENT APPLICATION: **US/10/808,121A**   TIME: 14:27:47

Input Set : **D:\V9661069.app**
Output Set: **N:\CRF4\08062004\J808121A.raw**

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264 <222> LOCATION: (2)...(1213)
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267 t aaa tgt agt aga atc ata cct gcg cgt gcg cgc gta gag tgt ttt gat   49
268   Lys Cys Ser Arg Ile Ile Pro Ala Arg Ala Arg Val Glu Cys Phe Asp
269   1                 5                 10                  15
271 aaa ttc aaa gtg aat tca aca cta gaa cag tat gtt ttc tgc act gta     97
272 Lys Phe Lys Val Asn Ser Thr Leu Glu Gln Tyr Val Phe Cys Thr Val
273               20                25                30
275 aat gca ttg cca gaa aca act gct gac att gta gtc ttt gat gaa atc    145
276 Asn Ala Leu Pro Glu Thr Thr Ala Asp Ile Val Val Phe Asp Glu Ile
277           35                40                45
279 tct atg gct act aat tat gac ttg agt gtt gtc aat gct aga ctt cgt    193
280 Ser Met Ala Thr Asn Tyr Asp Leu Ser Val Val Asn Ala Arg Leu Arg
281       50                55                60
283 gca aaa cac tac gtc tat att ggc gat cct gct caa tta cca gcc ccc    241
284 Ala Lys His Tyr Val Tyr Ile Gly Asp Pro Ala Gln Leu Pro Ala Pro
285 65                70                75                80
287 cgc aca ttg ctg act aaa ggc aca cta gaa cca gaa tat ttt aat tca    289
288 Arg Thr Leu Leu Thr Lys Gly Thr Leu Glu Pro Glu Tyr Phe Asn Ser
289               85                90                95
291 gtg tgc aga ctt atg aaa aca ata ggt cca gac atg ttc ctt gga act    337
292 Val Cys Arg Leu Met Lys Thr Ile Gly Pro Asp Met Phe Leu Gly Thr
293           100               105               110
295 tgt cgc cgt tgt cct gct gaa att gtt gac act gtg agt gct tta gtt    385
296 Cys Arg Arg Cys Pro Ala Glu Ile Val Asp Thr Val Ser Ala Leu Val
297           115               120               125
299 tat gac aat aag cta aaa gca cac aag gag aag tca gct caa tgc ttc    433
300 Tyr Asp Asn Lys Leu Lys Ala His Lys Glu Lys Ser Ala Gln Cys Phe
301       130               135               140
303 aaa atg ttc tac aaa ggt gtt att aca cat gat gtt tca tct gca atc    481
304 Lys Met Phe Tyr Lys Gly Val Ile Thr His Asp Val Ser Ser Ala Ile
305 145               150               155               160
307 aac aga cct caa ata ggc gtt gta aga gaa ttt ctt aca cgc aat cct    529
308 Asn Arg Pro Gln Ile Gly Val Val Arg Glu Phe Leu Thr Arg Asn Pro
309               165               170               175
311 gct tgg aga aaa gct gtt ttt atc tca cct tat aat tca cag aac gct    577
312 Ala Trp Arg Lys Ala Val Phe Ile Ser Pro Tyr Asn Ser Gln Asn Ala
313           180               185               190
315 gta gct tca aaa atc tta gga ttg cct acg cag act gtt gat tca tca    625
316 Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val Asp Ser Ser
317           195               200               205
319 cag ggt tct gaa tat gac tat gtc ata ttc aca caa act act gaa aca    673
320 Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr Thr Glu Thr
321       210               215               220
323 gca cac tct tgt aat gtc aac cgc ttc aat gtg gct atc aca agg gca    721
324 Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile Thr Arg Ala
325 225               230               235               240
327 aaa att ggc att ttg tgc ata atg tct gat aga gat ctt tat gac aaa    769
328 Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu Tyr Asp Lys
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/06/2004
PATENT APPLICATION: **US/10/808,121A**   TIME: 14:27:48

Input Set : **D:\V9661069.app**
Output Set: **N:\CRF4\08062004\J808121A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 21,22,23,24,25,26,27

VERIFICATION SUMMARY   DATE: 08/06/2004
PATENT APPLICATION: **US/10/808,121A**   TIME: 14:27:48

Input Set : **D:\V9661069.app**
Output Set: **N:\CRF4\08062004\J808121A.raw**

L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0